

1	CAAACTTGGT	GGCAACTTGC	CTCCCGGTGC	GGGCGTCTCT	CCCCCACCGT
51	CTCAA CATGC	TTAGGGGTCC	GGGGCCCGGG	CTGCTGCTGC	TGGCCGTCCA
101	GTGCCTGGGG	ACAGCGGTGC	CCTCCACGGG	AGCCTCGAAG	AGCAAGAGGC
151	AGGCTCAGCA	AATGGTTCAG	CCCCAGTCCC	CGGTGGCTGT	CAGTCAAAGC
201	AAGCCCGGTT	GTTATGACAA	TGGAAAACAC	TATCAGATAA	ATCAACAGTG
251	GGAGCGGACC	TACCTAGGCA	ATGCGTTGGT	TTGTACTTGT	TATGGAGGAA
301	GCCGAGGTTT	TAACTGCGAG	AGTAAACCTG	AAGCTGAAGA	GACTTGCTTT
351	GACAAGTACA	CTGGGAACAC	TTACCGAGTG	GGTGACACTT	ATGAGCGTCC
401	TAAAGACTCC	ATGATCTGGG	ACTGTACCTG	CATCGGGGCT	GGGCGAGGGA
451	GAATAAGCTG	TACCATCGCA	AACCGCTGCC	ATGAAGGGGG	TCAGTCCTAC
501	AAGATTGGTG	ACACCTGGAG	GAGACCACAT	GAGACTGGTG	GTTACATGTT
551	AGAGTGTGTG	TGTCTTGGTA	ATGGAAAAGG	AGAATGGACC	TGCAAGCCCA
601	TAGCTGAGAA	GTGTTTTGAT	CATGCTGCTG	GGACTTCCTA	TGTGGTCGGA
651	GAAACGTGGG	AGAAGCCCTA	CCAAGGCTGG	ATGATGGTAG	ATTGTACTTG
701	CCTGGGAGAA	GGCAGCGGAC	GCATCACTTG	CACTTCTAGA	AATAGATGCA
751	ACGATCAGGA	CACAAGGACA	TCCTATAGAA	TTGGAGACAC	CTGGAGCAAG
801	AAGGATAATC	GAGGAAACCT	GCTCCAGTGC	ATCTGCACAG	GCAACGGCCG
851	AGGAGAGTGG	AAGTGTGAGA	GGCACACCTC	TGTGCAGACC	ACATCGAGCG
901	GATCTGGCCC	CTTCACCGAT	GTTCGTGCAG	CTGTTTACCA	ACCGCAGCCT
951	CACCCCCAGC	CTCCTCCCTA	TGGCCACTGT	GTCACAGACA	GTGGTGTGGT
1001	CTACTCTGTG	GGGATGCAGT	GGCTGAAGAC	ACAAGGAAAT	AAGCAAATGC
1051	TTTGCACGTG	CCTGGGCAAC	GGAGTCAGCT	GCCAAGAGAC	AGCTGTAACC

## Fig. 1 (part 1)

SUBSTITUTE SHEET (RULE 26)



CAGACTTACG GTGGCAACTC AAATGGAGAG CCATGTGTCT TACCATTCAC 1151 CTACAACGAC AGGACGGACA GCACAACTTC GAATTATGAG CAGGACCAGA 1201 AATACTCTTT CTGCACAGAC CACACTGTTT TGGTTCAGAC TCGAGGAGGA AATTCCAATG GTGCCTTGTG CCACTTCCCC TTCCTATACA ACAACCACAA 1251 1301 TTACACTGAT TGCACTTCTG AGGGCAGAAG AGACAACATG AAGTGGTGTG 1351 GGACCACACA GAACTATGAT GCCGACCAGA AGTTTGGGTT CTGCCCCATG 1401 GCTGCCCACG AGGAAATCTG CACAACCAAT GAAGGGGTCA TGTACCGCAT 1451 TGGAGATCAG TGGGATAAGC AGCATGACAT GGGTCACATG ATGAGGTGCA 1501 CGTGTGTTGG GAATGGTCGT GGGGAATGGA CATGCATTGC CTACTCGCAG 1551 CTTCGAGATC AGTGCATTGT TGATGACATC ACTTACAATG TGAACGACAC 1601 ATTCCACAAG CGTCATGAAG AGGGGCACAT GCTGAACTGT ACATGCTTCG 1651 GTCAGGGTCG GGGCAGGTGG AAGTGTGATC CCGTCGACCA ATGCCAGGAT 1701 TCAGAGACTG GGACGTTTTA TCAAATTGGA GATTCATGGG AGAAGTATGT 1751 GCATGGTGTC AGATACCAGT GCTACTGCTA TGGCCGTGGC ATTGGGGAGT 1801 GGCATTGCCA ACCTTTACAG ACCTATCCAA GCTCAAGTGG TCCTGTCGAA 1851 GTATTTATCA CTGAGACTCC GAGTCAGCCC AACTCCCACC CCATCCAGTG 1901 GAATGCACCA CAGCCATCTC ACATTTCCAA GTACATTCTC AGGTGGAGAC 1951 CTGTGAGTAT CCCACCCAGA AACCTTGGAT ACTGAGTCTC CTAATCTTAT 2001 CAATTCTGAT GGTTTCTTTT TTTCCCAGCT TTTGAGCCAA CAACTCTGAT 2051 TAACTATTCC TATAGCATTT ACTATATTG TTTAGTGAAC AAACAATATG 2101 TGGTCAATTA AATTGACTTG TAGACTGAAA AAAAAAAAA AAAAAAA (SEQ ID NO.:

### Fig. 1 (part 2)

SUBSTITUTE SHEET (RULE 26)



CAAACTTGGT GGCAACTTGC CTCCCGGTGC GGGCGTCTCT CCCCCACCGT CTCAA CATGC TTAGGGGTCC GGGGCCCGGG CTGCTGCTGC TGGCCGTCCA 51 101 GTGCCTGGGG ACAGCGGTGC CCTCCACGGG AGCCTCGAAG AGCAAGAGGC AGGCTCAGCA AATGGTTCAG CCCCAGTCCC CGGTGGCTGT CAGTCAAAGC AAGCCCGGTT GTTATGACAA TGGAAAACAC TATCAGATAA ATCAACAGTG GGAGCGGACC TACCTAGGCA ATGCGTTGGT TTGTACTTGT TATGGAGGAA 251 301 GCCGAGGTTT TAACTGCGAG AGTAAACCTG AAGCTGAAGA GACTTGCTTT GACAAGTACA CTGGGAACAC TTACCGAGTG GGTGACACTT ATGAGCGTCC TAAAGACTCC ATGATCTGGG ACTGTACCTG CATCGGGGCT GGGCGAGGGA 401 GAATAAGCTG TACCATCGCA AACCGCTGCC ATGAAGGGGG TCAGTCCTAC 451 AAGATTGGTG ACACCTGGAG GAGACCACAT GAGACTGGTG GTTACATGTT 501 AGAGTGTGTG TGTCTTGGTA ATGGAAAAGG AGAATGGACC TGCAAGCCCA 551 TAGCTGAGAA GTGTTTTGAT CATGCTGCTG GGACTTCCTA TGTGGTCGGA 601 GAAACGTGGG AGAAGCCCTA CCAAGGCTGG ATGATGGTAG ATTGTACTTG 651 701 CCTGGGAGAA GGCAGCGGAC GCATCACTTG CACTTCTAGA AATAGATGCA ACGATCAGGA CACAAGGACA TCCTATAGAA TTGGAGACAC CTGGAGCAAG AAGGATAATC GAGGAAACCT GCTCCAGTGC ATCTGCACAG GCAACGGCCG AGGAGAGTGG AAGTGTGAGA GGCACACCTC TGTGCAGACC ACATCGAGCG 851 GATCTGGCCC CTTCACCGAT GTTCGTGCAG CTGTTTACCA ACCGCAGCCT 901 CTACTCTGTG GGGATGCAGT GGCTGAAGAC ACAAGGAAAT AAGCAAATGC 1001 TTTGCACGTG CCTGGGCAAC GGAGTCAGCT GCCAAGAGAC AGCTGTAACC 1051

## Fig. 1 (part 1)

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1101 CAGACTTACG GTGGCAACTC AAATGGAGAG CCATGTGTCT TACCATTCAC 1151 CTACAACGAC AGGACGGACA GCACAACTTC GAATTATGAG CAGGACCAGA 1201 AATACTCTTT CTGCACAGAC CACACTGTTT TGGTTCAGAC TCGAGGAGGA 1251 AATTCCAATG GTGCCTTGTG CCACTTCCCC TTCCTATACA ACAACCACAA 1301 TTACACTGAT TGCACTTCTG AGGGCAGAAG AGACAACATG AAGTGGTGTG 1351 GGACCACACA GAACTATGAT GCCGACCAGA AGTTTGGGTT CTGCCCCATG GCTGCCCACG AGGAAATCTG CACAACCAAT GAAGGGGTCA TGTACCGCAT TGGAGATCAG TGGGATAAGC AGCATGACAT GGGTCACATG ATGAGGTGCA CGTGTGTTGG GAATGGTCGT GGGGAATGGA CATGCATTGC CTACTCGCAG 1551 CTTCGAGATC AGTGCATTGT TGATGACATC ACTTACAATG TGAACGACAC 1601 ATTCCACAAG CGTCATGAAG AGGGGCACAT GCTGAACTGT ACATGCTTCG 1651 GTCAGGGTCG GGGCAGGTGG AAGTGTGATC CCGTCGACCA ATGCCAGGAT 1701 TCAGAGACTG GGACGTTTTA TCAAATTGGA GATTCATGGG AGAAGTATGT 1751 GCATGGTGTC AGATACCAGT GCTACTGCTA TGGCCGTGGC ATTGGGGAGT 1801 GGCATTGCCA ACCTTTACAG ACCTATCCAA GCTCAAGTGG TCCTGTCGAA GTATTTATCA CTGAGACTCC GAGTCAGCCC AACTCCCACC CCATCCAGTG GAATGCACCA CAGCCATCTC ACATTTCCAA GTACATTCTC AGGTGGAGAC 1951 CTGTGAGTAT CCCACCCAGA AACCTTGGAT ACTGAGTCTC CTAATCTTAT 2001 CAATTCTGAT GGTTTCTTTT TTTCCCAGCT TTTGAGCCAA CAACTCTGAT 2051 TAACTATTCC TATAGCATTT ACTATATTG TTTAGTGAAC AAACAATATG 2101 TGGTCAATTA AATTGACTTG TAGACTGAAA AAAAAAAAA AAAAAAA (SEQ 1D NO.: 2)\_\_\_

### Fig. 1 (part 2)

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		3	<i>1 1</i>			
	10	20	30	40	50	60
MSF-1α	NLVATCLPVRASLE	HRLMMLRGP	GPGLLLLAVQ	CLGTAVPST	ASKSKRQAQQ	MVQPQSP
		11111111				
fibronectin	NLVATCLPVRASLI	PHRLNMLRGP	GPGLLLLAVQ 10	CLGTAVPSTO 20	SASKSKRQAQQ 30	
			10	20	30	40
	70	80	90	100	110	120
MSF-1α	VAVSQSKPGCYDNO	KHYQINQQW	ERTYLGNALV	CTCYGGSRGI	FNCESKPEAEE	TCFDKYT
			11111111:11		11111111111	$\Pi\Pi\Pi\Pi$
fibronectin	VAVSQSKPGCYDNO	-				TCFDKYT
	50	60	70	80	90	100
	130	140	150	160	170	180
MOD 1 **	GNTYRVGDTYERPI					
MSF-1α	IIIIIIIIIIIIII					
fibronectin	GNTYRVGDTYERPI	KDSMIWDCTC				
	110	120	130	140	150	160
	190	200	210	220	230	240
MSF-1α	YMLECVCLGNGKG	EWTCKPIAE	CFDHAAGTSY	VVGETWEKP	YQGWMMVDCT	CLGEGSGR
<i>6:</i> 1			 CTCV	 		
Ilbronectin	170	180	190	200	210	220
	170	100				
	250	260	270	280	290	300
MSF-1α	ITCTSRNRCNDQD'	TRTSYRIGDT	TWSKKDNRGNL	LQCICTGNG	RGEWKCERHTS	SVQTTSSG
		1111111111				
fibronectin	ITCTSRNRCNDQD					
	230	240	250	260	270	280
	310	320	330	340	350	360
MSF-1α	SGPFTDVRAAVYQ			YSVGMOWLK	TOGNKOMLCT	CLGNGVSC
fibronectin	SGPFTDVRAAVYQ	PQPHPQPPP	YGHCVTDSGVV	/YSVGMQWLK	TQGNKQMLCT	CLGNGVSC
	290	300	310	320	330	340
	370	200			390	400
WGE 1	370	380	TUNIDDT			400 DOVVERCT
MSF-1α	QETAVTQTYGGNS				-D3113M1EQ	
fibronectin	QETAVTQTYGGNS			TTEGRQDGHL		
	350	360	370	380	390	400
				440		460
MSF-1α	DHTVLVQTRGGNS				-	-
fibropection						, , , , , , , ,
TIDIONECCII	410	420	430	440	450	460

## Fig. 2 (part 1)



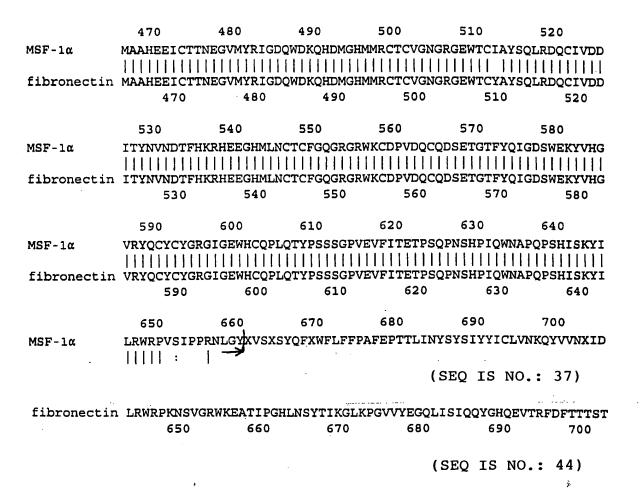


Fig. 2 (part 2)

#### PCT/GB98/03766



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	10	20	30	40	50	60
MSF-1α	NLVATCLPVRASLP	HRLNMLRGP	GPGLLLLAVQ	CLGTAVPST	Gaskskrqaqq	MVQPQSP
fibranastin						
ribronectin	NLVATCLPVRASLP	HKTWMTKGP	GPGLLLLLAVQI 10	CLGTAVPSTO 20	GASKSKRQAQQ 30	MVQPQSP 40
						40
	70	80	90	100	. 110	120
MSF-1α	VAVSQSKPGCYDNG					TCFDKYT
fibronectin	VAVSQSKPGCYDNG					
2201011001111	50	60	70	80	PNCESRPEAEE 90	100
	130	140	150	160	170	180
MSF-1α	GNTYRVGDTYERPK	DSMIWDCTC				RPHETGG
fibronectin	GNTYRVGDTYERPK	 DSMIWDCTC	TGAGRGRISC			PREE
	110	120	130	140	150	160
	190	200	210	220	230	240
MSF-1α	YMLECVCLGNGKGE	WTCKPIAEK		VVGETWEKP	YQGWMMVDCTC	LGEGSGR
fibronectin	YMLECVCLGNGKGE		 CFDHAAGTSY		YOGWMMVDCTC	
	170	180	190	200	210	220
	250	260	270	280	290	300
MSF-1α	ITCTSRNRCNDQDT		WSKKDNRGNL 			VQTTSSG
fibronectin	ITCTSRNRCNDQDI					VOTTSSG
•	230	240	250	260	270	280
	210	200	222	240		
MSF-1α	310	320	330	340 XCVCNOWI K	350	360
MSF-14	SGPFTDVRAAVYQF					
fibronectin	SGPFTDVRAAVYQF					
	290	300	310	320	330	340
	370	380			390 4	
MSF-1α	QETAVTQTYGGNSN		'VNDPT			100
						-
fibronectin	QETAVTQTYGGNSN	GEPCVLPFI	TYNGRTFYSCT	TEGRQDGHL	WCSTTSNYEQI	OCKYSFCT
	350	360	370	380	390	400
	410 42	20 4	130 4	40	450	160
MSF-1α	DHTVLVQTRGGNSN					
		[]]]]]		1111111	11111111111	11111111
fibronectin	DHTVLVQTQGGNSN	NGALCHFPFI	LYNNHNYTDCI	SEGRRDNMK	WCGTTQNYDA	DOKFGFCP
	410	420	430	440	450	460

# Fig. 2 (part 1)



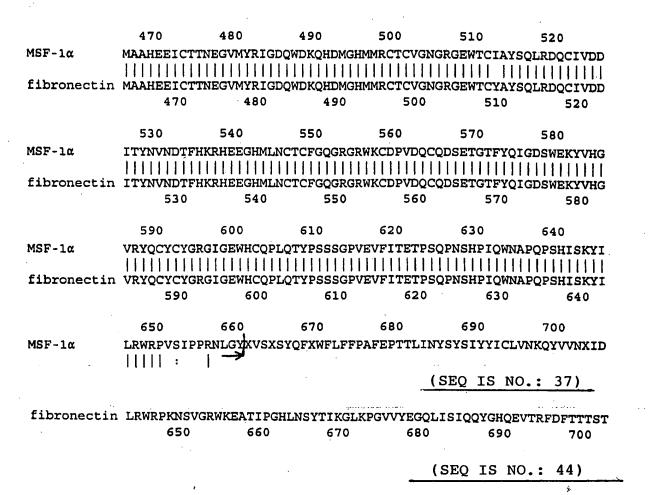


Fig. 2 (part 2)